

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/116,676DATE: 07/21/98
TIME: 14:20:11

INPUT SET: S27568.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
23 (1) General Information:
45 (i) APPLICANT: Borowsky, Beth
67 (ii) TITLE OF INVENTION: DNA ENCODING A HUMAN Ob RECEPTOR
8 (hOb-Re) AND USES THEREOF
910 (iii) NUMBER OF SEQUENCES: 29
1112 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Cooper & Dunham LLP
14 (B) STREET: 1185 Avenue of the Americas
15 (C) CITY: New York
16 (D) STATE: New York
17 (E) COUNTRY: USA
18 (F) ZIP: 10036
1920 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
2526 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
3031 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: White, John P
33 (B) REGISTRATION NUMBER: 28,678
34 (C) REFERENCE/DOCKET NUMBER: 1795-53801/JPW/KDB
3536 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 212 278 0400
38 (B) TELEFAX: 212 291 0525
3940 (2) INFORMATION FOR SEQ ID NO:1:
4142 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 54 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
46

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/116,676DATE: 07/21/98
TIME: 14:20:12

INPUT SET: S27568.raw

47 (D) TOPOLOGY: linear
48
49 (ii) MOLECULE TYPE: DNA
50
51 (ix) FEATURE:
52 (A) NAME/KEY: CDS
53 (B) LOCATION: 1..54
54
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57 AAT GTT AAA AAG TTT CAC ATC CAC GGT ATG TGT ACT GTA CTT TTC ATG 48
58 Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met
59 1 5 10 15
60
61 GAT TAG 54
62 Asp *
63
64
65
66 (2) INFORMATION FOR SEQ ID NO:2:
67
68 (i) SEQUENCE CHARACTERISTICS:
69 (A) LENGTH: 17 amino acids
70 (B) TYPE: amino acid
71 (D) TOPOLOGY: linear
72
73 (ii) MOLECULE TYPE: protein
74
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
76
77 Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met
78 1 5 10 15
79
80 Asp
81
82
83
84 (2) INFORMATION FOR SEQ ID NO:3:
85
86 (i) SEQUENCE CHARACTERISTICS:
87 (A) LENGTH: 45 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: single
90 (D) TOPOLOGY: linear
91
92 (ii) MOLECULE TYPE: DNA
93
94 (ix) FEATURE:
95 (A) NAME/KEY: CDS
96 (B) LOCATION: 1..45
97
98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
99

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/116,676DATE: 07/21/98
TIME: 14:20:13

INPUT SET: S27568.raw

100 TCT GTT AAG AAG TAT TAT ATC CAT GGT AAG TTT ACT ATA CTT TAG 45
101 Ser Val Lys Lys Tyr Tyr Ile His Gly Lys Phe Thr Ile Leu *
102 1 5 10 15
103
104
105 (2) INFORMATION FOR SEQ ID NO:4:

106
107 (i) SEQUENCE CHARACTERISTICS:
108 (A) LENGTH: 14 amino acids
109 (B) TYPE: amino acid
110 (D) TOPOLOGY: linear
111

112 (ii) MOLECULE TYPE: protein
113
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

115
116 Ser Val Lys Lys Tyr Tyr Ile His Gly Lys Phe Thr Ile Leu
117 1 5 10 15

118
119
120 (2) INFORMATION FOR SEQ ID NO:5:

121
122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 27 base pairs
124 (B) TYPE: nucleic acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: linear
127

128 (ii) MOLECULE TYPE: DNA
129
130

131 (ix) FEATURE:
132 (A) NAME/KEY: CDS
133 (B) LOCATION: 1..27
134
135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
136

137 GGT ATG TGT ACT GTA CTT TTC ATG GAT 27
138 Gly Met Cys Thr Val Leu Phe Met Asp
139 1 5

140
141
142 (2) INFORMATION FOR SEQ ID NO:6:

143
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 9 amino acids
146 (B) TYPE: amino acid
147 (D) TOPOLOGY: linear
148

149 (ii) MOLECULE TYPE: protein
150
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
152

INPUT SET: S27568.raw

153 Gly Met Cys Thr Val Leu Phe Met Asp
154 1 5

155

156

157 (2) INFORMATION FOR SEQ ID NO:7:

158

159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 18 base pairs
161 (B) TYPE: nucleic acid
162 (C) STRANDEDNESS: single
163 (D) TOPOLOGY: linear

164

165 (ii) MOLECULE TYPE: DNA

166

167 (ix) FEATURE:

168 (A) NAME/KEY: CDS
169 (B) LOCATION: 1..18

170

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

172

173 GGT AAG TTT ACT ATA CTT
174 Gly Lys Phe Thr Ile Leu
175 10 15

18

176

177

178

179 (2) INFORMATION FOR SEQ ID NO:8:

180

181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 6 amino acids
183 (B) TYPE: amino acid
184 (D) TOPOLOGY: linear

185

186 (ii) MOLECULE TYPE: protein

187

188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

189

190 Gly Lys Phe Thr Ile Leu
191 1 5

192

193

194

195 (2) INFORMATION FOR SEQ ID NO:9:

196

197 (i) SEQUENCE CHARACTERISTICS:
198 (A) LENGTH: 2415 base pairs
199 (B) TYPE: nucleic acid
200 (C) STRANDEDNESS: single
201 (D) TOPOLOGY: linear

202

203 (ii) MOLECULE TYPE: DNA

204

205 (ix) FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/116,676

INPUT SET: S27568.raw

206 (A) NAME/KEY: CDS
207 (B) LOCATION: 1..2415
208
209 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
210
211 ATG ATT TGT CAA AAA TTC TGT GTG GTT TTG TTA CAT TGG GAA TTT ATT 48
212 Met Ile Cys Gln Lys Phe Cys Val Val Leu Leu His Trp Glu Phe Ile
213 1 5 10 15
214
215 TAT GTG ATA ACT GCG TTT AAC TTG TCA TAT CCA ATT ACT CCT TGG AGA 96
216 Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
217 20 25 30
218
219 TTT AAG TTG TCT TGC ATG CCA CCA AAT TCA ACC TAT GAC TAC TTC CTT 144
220 Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu
221 35 40 45
222
223 TTG CCT GCT GGA CTC TCA AAG AAT ACT TCA AAT TCG AAT GGA CAT TAT 192
224 Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
225 50 55 60
226
227 GAG ACA GCT GTT GAA CCT AAG TTT AAT TCA AGT GGT ACT CAC TTT TCT 240
228 Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
229 65 70 75 80
230
231 AAC TTA TCC AAA ACA ACT TTC CAC TGT TGC TTT CGG AGT GAG CAA GAT 288
232 Asn Leu Ser Lys Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
233 85 90 95
234
235 AGA AAC TGC TCC TTA TGT GCA GAC AAC ATT GAA GGA AAG ACA TTT GTT 336
236 Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val
237 100 105 110
238
239 TCA ACA GTA AAT TCT TTA GTT TTT CAA CAA ATA GAT GCA AAC TGG AAC 384
240 Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
241 115 120 125
242
243 ATA CAG TGC TGG CTA AAA GGA GAC TTA AAA TTA TTC ATC TGT TAT GTG 432
244 Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
245 130 135 140
246
247 GAG TCA TTA TTT AAG AAT CTA TTC AGG AAT TAT AAC TAT AAG GTC CAT 480
248 Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
249 145 150 155 160
250
251 CTT TTA TAT GTT CTG CCT GAA GTG TTA GAA GAT TCA CCT CTG GTT CCC 528
252 Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
253 165 170 175
254
255 CAA AAA GGC AGT TTT CAG ATG GTT CAC TGC AAT TGC AGT GTT CAT GAA 576
256 Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
257 180 185 190
258

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/116,676

DATE: 07/21/98
TIME: 14:20:16

INPUT SET: S27568.raw

Line	Error	Original Text
80	Stop Codon at end of sequence removed - no error	
116	Stop Codon at end of sequence removed - no error	
577	Stop Codon at end of sequence removed - no error	